RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
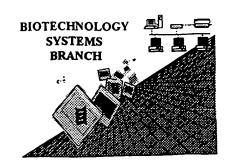BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/834,794_

Source: _OIPE_

Date Processed by STIC: _5/8 /2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _09/834,294_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics — The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 ____ Wrapped Aminos — The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 ____ Incorrect Line Length — The rules require that a line not exceed 72 characters in length. This includes spaces.

4 ____ Misaligned Amino Acid Numbering — The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 ____ Non-ASCII — This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 ____ Variable Length — Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 ____ PatentIn ver. 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 ____ Skipped Sequences (OLD RULES) — Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 ____ Skipped Sequences (NEW RULES) — Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

11 ____ Use of "Artificial" (NEW RULES) — Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.

12 ____ Use of <220>Feature (NEW RULES) — Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 ____ PatentIn ver. 2.0 "bug" — **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

```
        RAW SEQUENCE LISTING              DATE: 05/08/2001
        PATENT APPLICATION:  US/09/834,794    TIME: 15:44:28

        Input Set : A:\Seqlist.txt
        Output Set: N:\CRF3\05082001\I834794.raw
```

Does Not Comply
Corrected Diskette Needed

~~~ (handwritten: PPI-5)

```
 3 <110> APPLICANT: Lawrence, Papsidero
 4         Lyn, Dyster
 5         Jana, Frustaci
 7 <120> TITLE OF INVENTION: Detection and Treatment of Breast Cancer
 9 <130> FILE REFERENCE: 3380/1I127-US4
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/834,794
C--> 12 <141> CURRENT FILING DATE: 2001-04-13
14 <150> PRIOR APPLICATION NUMBER: 09/146,580
15 <151> PRIOR FILING DATE: 1998-09-03
17 <150> PRIOR APPLICATION NUMBER: 60/071,899
18 <151> PRIOR FILING DATE: 1998-01-20
20 <150> PRIOR APPLICATION NUMBER: 60/092,155
21 <151> PRIOR FILING DATE: 1998-07-09
23 <160> NUMBER OF SEQ ID NOS: 35
25 <170> SOFTWARE: PatentIn version 3.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 127
29 <212> TYPE: PRT
30 <213> ORGANISM: Homo sapiens
32 <220> FEATURE:
33 <221> NAME/KEY: UNSURE
34 <222> LOCATION: (70)..(70)
35 <223> OTHER INFORMATION: Xaa at position 70 is either Arg or Gly
38 <220> FEATURE:
39 <221> NAME/KEY: UNSURE
40 <222> LOCATION: (91)..(91)
41 <223> OTHER INFORMATION: Xaa at position 70 is either Lys or Asn
44 <400> SEQUENCE: 1
46 Met Gln Gln Arg Gly Leu Ala Ile Val Ala Leu Ala Val Cys Ala Ala
47 1               5                   10                  15
49 Leu His Ala Ser Glu Ala Ile Leu Pro Ile Ala Ser Ser Cys Cys Thr
50              20                  25                  30
52 Glu Val Ser His His Ile Ser Arg Arg Leu Leu Glu Arg Val Asn Met
53              35                  40                  45
55 Cys Arg Ile Gln Arg Ala Asp Gly Asp Cys Asp Leu Ala Ala Val Ile
56        50                  55                  60
58 Leu His Val Lys Arg Xaa Arg Ile Cys Val Ser Pro His Asn His Thr
59 65                  70                  75                  80
61 Val Lys Gln Trp Met Lys Val Gln Ala Ala Xaa Lys Asn Gly Lys Gly
62              85                  90                  95
64 Asn Val Cys His Arg Lys Lys His His Gly Lys Arg Asn Ser Asn Arg
65              100                 105                 110
67 Ala His Gln Gly Lys His Glu Thr Tyr Gly His Lys Thr Pro Tyr
68              115                 120                 125
70 <210> SEQ ID NO: 2
71 <211> LENGTH: 104
72 <212> TYPE: PRT
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(handwritten annotations: "91 (see below)" near line 40; "OK" near line 58; circled "70" at line 61; circled "Xaa" at line 61)

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 73 <213> ORGANISM: Homo sapiens
 75 <220> FEATURE:
 76 <221> NAME/KEY: UNSURE
 77 <222> LOCATION: (47)..(47)
 78 <223> OTHER INFORMATION: Xaa at position 47 is either Arg or Gly
 81 <220> FEATURE:
 82 <221> NAME/KEY: UNSURE
 83 <222> LOCATION: (68)..(68)
 84 <223> OTHER INFORMATION: Xaa at position 47 is either Lys or Asn
 87 <400> SEQUENCE: 2
 89 Leu Pro Ile Ala Ser Ser Cys Cys Thr Glu Val Ser His His Ile Ser
 90 1               5                   10                  15
 92 Arg Arg Leu Leu Glu Arg Val Asn Met Cys Arg Ile Gln Arg Ala Asp
 93             20                  25                  30
 95 Gly Asp Cys Asp Leu Ala Ala Val Ile Leu His Val Lys Arg Xaa Arg
 96             35                  40                  45
 98 Ile Cys Val Ser Pro His Asn His Thr Val Lys Gln Trp Met Lys Val
 99       50                  55                  60
101 Gln Ala Ala Xaa Lys Asn Gly Lys Gly Asn Val Cys His Arg Lys Lys
102 65                  70                  75                  80
104 His His Gly Lys Arg Asn Ser Asn Arg Ala His Gln Gly Lys His Glu
105             85                  90                  95
107 Thr Tyr Gly His Lys Thr Pro Tyr
108             100
110 <210> SEQ ID NO: 3
111 <211> LENGTH: 18
112 <212> TYPE: PRT
113 <213> ORGANISM: Homo sapiens
115 <400> SEQUENCE: 3
117 Thr Glu Val Ser His His Ile Ser Arg Arg Leu Leu Glu Arg Val Asn
118 1               5                   10                  15
120 Met Cys
123 <210> SEQ ID NO: 4
124 <211> LENGTH: 16
125 <212> TYPE: PRT
126 <213> ORGANISM: Homo sapiens
128 <400> SEQUENCE: 4
130 Lys Asn Gly Lys Gly Asn Val Cys His Arg Lys Lys His His Gly Lys
131 1               5                   10                  15
133 <210> SEQ ID NO: 5
134 <211> LENGTH: 19
135 <212> TYPE: PRT
136 <213> ORGANISM: Homo sapiens
138 <400> SEQUENCE: 5
140 Asn Ser Asn Arg Ala His Gln Gly Lys His Glu Thr Tyr Gly His Lys
141 1               5                   10                  15
143 Thr Pro Tyr
146 <210> SEQ ID NO: 6
147 <211> LENGTH: 3117
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68 (see below)

OK

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       148 <212> TYPE: DNA
       149 <213> ORGANISM: Homo sapiens
       151 <220> FEATURE:
       152 <221> NAME/KEY: unsure                line exceeds 72-character-limit ( see item 3
       153 <222> LOCATION: (1)..(3117)                                        on Error summary
       154 <223> OTHER INFORMATION: n at any position in the sequence may represent a or g or c or t/
       158 <400> SEQUENCE: 6
W--> 159 aacatcctca cttgtgttgc tgtcagtgcc tgtanggcag gcaggaatgc agcagagagg    60
     161 actcgccatc gtggccttgg ctgtctgtgc ggccctacat gcctcagaag ccatacttcc   120
     163 cattgcctcc agctgttgca cggaggtttc acatcatatt tccagaaggc tcctggaaag   180
     165 agtgaatatg tgtcgcatcc agagagctga tggggattgt gacttggctg ctgtcatcct   240
W--> 167 tcatgtcaag cgcngaagaa tctgtgtcag cccgcacaac catactgtta agcagtggat   300
W--> 169 gaaagtgcaa gctgccaana aaaatggtaa aggaaatgtt tgccacagga agaaacacca   360
     171 tggcaagagg aacagtaaca gggcacatca ggggaaacac gaaacatacg gccataaaac   420
     173 tccttattag agaatctaca gataaatcta cagagacaat cccccaagtg gacttggcca   480
     175 tgattggttg taagtttatc atctgaattc tccttattgt agacaacaga acaaaacaaa   540
     177 atattggttt ttaaaaaatg aacaattgtg ccgtatgcaa atgtacccaa taatatactc   600
W--> 179 cactggaaaa tgaaatgaaa aaannatact ggctgggtat ggtgggtccc cccttttatc   660
. W-r-> 181 ccannnnctt cgggaggcag aggcaggagg atcacttgag accaggantt ngagacnagc   720
\W-> 183 tnggggcaaa anagcaanga cntcatttnt acaaacnaaa aaaaannttg gcccggcntg   780
W-> 185 gtagnacttg cntataatcc cagcnacatg ggaggtngag gtgggaggat cacttgagtc   840
W-> 187 tgggngagtt ngaggtngca gtgagcagcn tgggtgacag aatgnagacc ntgtctctaa   900
W-> 189 aaataataat aataatgata gtgtatatct tcatataata ttttaagnag gagcatatag   960
W-> 191 atataacttn ctcccaactt tttaattata gttttccaaa cttacagaga agttaaaaga  1020
     193 atggtacaat gaacatctat atatctttca ccacaatatt aatcattgtt aatattgtgc  1080
W--> 195 cacatttgct ttctctctcc tctcttggta ggggttncaa tataaaatat tataactttt  1140
     197 aaaatatatc ttgttttgct aaccattgga aaataagttg caaaaatcat gacacttcac  1200
W--> 199 ccctagtttc ttttnggtgt tataacttga catacccctaa aataaagaca tttttctaca  1260
     201 taatcacctt atcagtttta tacctaaaaa attaataatt tcatctaata tattccatat  1320
     203 tcaaattttc ccaactattt agagagcatt ttatgtagtt tttttttcac tccagtaatc  1380
W--> 205 aatcaaggtn gacatacata ttgcaaataa ttgttatttt tctttaatat ctttcaatct  1440
     207 aagaaagttc ctctgtcttt tttttttaat ttttaaaatt attttgttga gggagggtct  1500
     209 tgctgtgtct tccaggctgg agtgcagtgg cacaattttg attttggctc actgaagcct  1560
W--> 211 caactttagg gctcaagcaa tcctcccacc tcagcctncc cgagtatctg ggatcaaggt  1620
     213 gcatacccac cacacctggc taattttgtt tattttttgt agagacaggg tctcactatg  1680
     215 ttgcccaggt tgatctcaaa ctcctgggct caagcgatcc tcccacctta gcctcccaaa  1740
     217 gtactgggat tataggtgtg agccacagtg cctggcctaa ttattttctt gtgatcaaat  1800
     219 tcaggtttaa tgtttttggt taagaatttc ctacgtgaat tcgtgtactt attttgtcat  1860
     221 ttagagttca taaatattag ggtttatttt ctaaatagaa tagtttaaac taaatataac  1920
     223 ttcaaaacgt ctagtttgag tagctaccgt tgtttggatt gaaattttct gatactgaaa  1980
W--> 225 agaacaaaaa gcctgccttt ctgcccanaa csnnttgcyt cccccagtna gttcttggng  2040
W--> 227 cagnactagt tagggnccca gagttnggcc ttnngkgtgg tgatttrang ytctgcctaa  2100
W--> 229 acaaggngcn wacatyrttt agctcctatt ccaccyttct namamgtttt tgttgtkgtt  2160
W--> 231 tgnttgtttt tttkgagaca grrtntnayt ctgtttgccc argctggart tgcagtggca  2220
W--> 233 caatytnggy tncattgcaa cytcngcytc cssgccgttc aaktgatyyt cttgcytcag  2280
W--> 235 cytccccaag taantgatat tacaggngcc cagccaccam accccgntga wttttgtatt  2340
W--> 237 tttartarar amrgggtttt cccgcnttgg cngggctggt ctcnaantcc ttgamctcna  2400
W--> 239 ktgaaccacc cgcctgtgcc ycccaaantg ctggaattac cancgttgan ccaccatgcc  2460
W--> 241 gggcycacac gtttgarttt ganaccattg tnccattcct cttttggcct yttttttntc  2520
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W--> 243  catagnngct tcaagataga tangtaagrg cccagtagtn gttcwtarga agcnmatagr  2580
W--> 245  rancrggarc cantttnatc aggtgggcag gtgtccnngg cytccctgct ggytnntccc  2640
W--> 247  aagcggtggt gttgccarga nktnttggar gtgataatgg gananaccag naggcmctga  2700
W--> 249  gtyncnntag gttnaaatgc caccaaaact ggcctttggc ctaatatccy ycnttgamta  2760
W--> 251  nttarcattt awtttattwa tttncctgac atttntgcma ncctttgtwt ttntatttcc  2820
W--> 253  nctntatara wgargaaatt tgaggntytt araggtaaaa tganttgcnc nrgtnnacmc  2880
W--> 255  aggaagtggc nraranaanc tttttanatn mgaaaaaatt aataaaatat aatatgagag  2940
     257  taacttaaaa tattaataaa ccacaatttt aaattaatta accgtgataa ccaacattaa  3000
W--> 259  taaaagttaa gataccaaaa cactggtgtn taatttttn aactaacaan ttgaattatt  3060
W--> 261  ttccatttta aattaattaa ccgtgataac caacattaat aaaagttaag ataccgn     3117
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     265  <211> LENGTH: 381
     266  <212> TYPE: DNA
     267  <213> ORGANISM: Homo sapiens
     269  <220> FEATURE:
     270  <221> NAME/KEY: unsure
     271  <222> LOCATION: (207)..(207)
     272  <223> OTHER INFORMATION: n may represent a or g or c or t/u
     275  <220> FEATURE:
     276  <221> NAME/KEY: unsure
     277  <222> LOCATION: (272)..(272)
     278  <223> OTHER INFORMATION: n may represent a or g or c or t/u
     281  <400> SEQUENCE: 7
     282  atgcagcaga gaggactcgc catcgtggcc ttggctgtct gtgcggccct acatgcctca   60
     284  gaagccatac ttcccattgc ctccagctgt tgcacggagg tttcacatca tatttccaga  120
     286  aggctcctgg aaagagtgaa tatgtgtcgc atccagagag ctgatgggga ttgtgacttg  180
W--> 288  gctgctgtca tccttcatgt caagcgggga agaatctgtg tcagcccgca caaccatact  240
W--> 290  gttaagcagt ggatgaaagt gcaagctgcc aanaaaaatg gtaaaggaaa tgtttgccac  300
     292  aggaagaaac accatggcaa gaggaacagt aacagggcac atcagggaa acacgaaaca  360
     294  tacggccata aaactcctta t                                             381
     297  <210> SEQ ID NO: 8
     298  <211> LENGTH: 104
     299  <212> TYPE: DNA
     300  <213> ORGANISM: Homo sapiens
     302  <400> SEQUENCE: 8
     303  acacgaattc acgtaggaaa ttcttaacca aaaacattaa acctgaattt gatcacaaga   60
     305  aaataattag gccaggcact gtggctcaca cctataatcc cagt                   104
     308  <210> SEQ ID NO: 9
     309  <211> LENGTH: 25
     310  <212> TYPE: DNA
     311  <213> ORGANISM: Homo sapiens
     313  <400> SEQUENCE: 9
     314  gaattcacgt aggaaattct taacc                                         25
     317  <210> SEQ ID NO: 10
     318  <211> LENGTH: 22
     319  <212> TYPE: DNA
     320  <213> ORGANISM: Homo sapiens
     322  <400> SEQUENCE: 10
     323  actgggatta taggtgtgag cc                                            22
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Handwritten annotations: (208)..(208) "c" is at location 207; (273)..(273) "a" is at location 272

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326 <210> SEQ ID NO: 11
327 <211> LENGTH: 311
328 <212> TYPE: DNA
329 <213> ORGANISM: Homo sapiens
331 <220> FEATURE:
332 <221> NAME/KEY: unsure
333 <222> LOCATION: (101)..(101)
334 <223> OTHER INFORMATION: n may be a or g or c or t/u
337 <220> FEATURE:
338 <221> NAME/KEY: unsure
339 <222> LOCATION: (162)..(162)
340 <223> OTHER INFORMATION: n may be a or g or c or t/u
343 <400> SEQUENCE: 11
344 ggagagagcc gtatgtttcg tgtttccct gatgtgccct gttactgttc ctcttgccat      60
346 ggtgtttctt cctgtggcaa acatttcctt taccattttt nttggcagct tgcactttca     120
348 tccactgctt aacagtatgg ttgtgcgggc tgacacagat tnttctgcgc ttgacatgaa     180
350 ggatgacagc agccaagtca caatccccat cagctctctg gatgcgacac atattcactc     240
352 tttccaggag ccttctggaa atatgatgtg aaacctccgt gcaacagctg gaggcaatgg     300
354 gaagtatggc t                                                          311
357 <210> SEQ ID NO: 12
358 <211> LENGTH: 20
359 <212> TYPE: DNA
360 <213> ORGANISM: Artificial
362 <220> FEATURE:
363 <223> OTHER INFORMATION: Sequencing primer T7
365 <400> SEQUENCE: 12
366 taatacgact cactataggg                                                  20
369 <210> SEQ ID NO: 13
370 <211> LENGTH: 18
371 <212> TYPE: DNA
372 <213> ORGANISM: Artificial
374 <220> FEATURE:
375 <223> OTHER INFORMATION: pCR3.1 Reverse Primer
377 <400> SEQUENCE: 13
378 tagaaggcac agtcgagg                                                    18
381 <210> SEQ ID NO: 14
382 <211> LENGTH: 22
383 <212> TYPE: DNA
384 <213> ORGANISM: Artificial
386 <220> FEATURE:
387 <223> OTHER INFORMATION: Gene specific primer (24R)
389 <400> SEQUENCE: 14
390 actgggatta taggtgtgag cc                                               22
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394 <211> LENGTH: 24
395 <212> TYPE: DNA
396 <213> ORGANISM: Artificial
398 <220> FEATURE:
399 <223> OTHER INFORMATION: Gene specific primer (24R2)
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C--> 360
C--> 372
C--> 384
C--> 396

See item 11 on Error Summary Sheet

The types of errors shown exist <u>throughout</u> the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY   DATE: 05/08/2001
PATENT APPLICATION: US/09/834,794   TIME: 15:44:29

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\05082001\I834794.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:58 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:61 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:95 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
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L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:211 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:225 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
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L:249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:251 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:253 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:255 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:261 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:288 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:290 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:360 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:372 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:384 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:396 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:408 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:420 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/834,794

DATE: 05/08/2001
TIME: 15:44:29

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\05082001\I834794.raw

L:432 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:444 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19